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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/020,618

DATE: 04/17/2002
TIME: 11:53:16

Input Set : N:\Crf3\RULE60\10020618.raw
Output Set: N:\CRF3\04172002\J020618.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: Bandman, Olga
Goli, Surya K.
(ii) TITLE OF INVENTION: A NOVEL H-REV107-LIKE PROTEIN
(iii) NUMBER OF SEQUENCES: 4
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
(vi) CURRENT APPLICATION DATA:
C--> (A) APPLICATION NUMBER: US/10/020,618
C--> (B) FILING DATE: 06-Dec-2001
(C) CLASSIFICATION:
(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/801,742
(B) FILING DATE:
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0200 US
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415-855-0555
(B) TELEFAX: 415-845-4166
(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
Met Ala Ser Pro His Gln Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
 1               5                  10                  15
Phe Arg Leu Gly Tyr Glu His Trp Ala Leu Tyr Ile Gly Asp Gly Tyr
```

ENTERED

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```
                20                  25                  30
Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser
        35                  40                  45
Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Glu Arg
    50                  55                  60
Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu
65                  70                  75                  80
Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala
                85                  90                  95
Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn
            100                 105                 110
Cys Glu His Phe Val Thr Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys
        115                 120                 125
Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly
    130                 135                 140
W--> Ile Leu Val Val Ala Gly Cys Ser Phe Xaa Ile Arg Arg Tyr Gln Lys
145                 150                 155                 160
Lys Ala Thr Ala
```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 577 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
AAACAAGAGG AGCACCAGAC CTCCTCTTGG CTTCGAGATG GCTTCGCCAC ACCAAGAGCC     60
CAAACCTGGA GACCTGATTG AGATTTTCCG CCTTGGCTAT GAGCACTGGG CCCTGTATAT    120
AGGAGATGGC TACGTGATCC ATCTGGCTCC TCCAAGTGAG TACCCCGGGG CTGGCTCCTC    180
CAGTGTCTTC TCAGTCCTGA GCAACAGTGC AGAGGTGAAA CGGGAGCGCC TGGAAGATGT    240
GGTGGGAGGC TGTTGCTATC GGGTCAACAA CAGCTTGGAC CATGAGTACC AACCACGGCC    300
CGTGGAGGTG ATCATCAGTT CTGCGAAGGA GATGGTTGGT CAGAAGATGA AGTACAGTAT    360
TGTGAGCAGG AACTGTGAGC ACTTTGTCAC CCAGCTGAGA TATGGCAAGT CCCGCTGTAA    420
ACAGGTGGAA AAGGCCAAGG TTGAAGTCGG TGTGGCCACG GCGCTTGGAA TCCTGGTTGT    480
TGCTGGATGC TCTTTTGNGA TTAGGAGATA CCAAAAAAAA GCGACAGCCT GAAGCAGCCA    540
CAAAATCCTG TGTTAGAAGC AGCTGTGGGG GTCCCAA                             577
```

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 162 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 1054752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
Met Arg Ala Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile
 1               5                  10                  15
Phe Arg Pro Phe Tyr Arg His Trp Ala Ile Tyr Val Gly Asp Gly Tyr
            20                  25                  30
```

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PATENT APPLICATION: US/10/020,618 TIME: 11:53:16

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```
Val Val His Leu Ala Pro Pro Ser Glu Val Ala Gly Ala Gly Ala Ala
          35                  40                  45
Ser Val Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu
      50                  55                  60
Leu Tyr Asp Val Ala Gly Ser Asp Lys Tyr Gln Val Asn Asn Lys His
65                  70                  75                  80
Asp Asp Lys Tyr Ser Pro Leu Pro Cys Thr Lys Ile Ile Gln Arg Ala
                85                  90                  95
Glu Glu Leu Val Gly Gln Glu Val Leu Tyr Lys Leu Thr Ser Glu Asn
            100                 105                 110
Cys Glu His Phe Val Asn Glu Leu Arg Tyr Gly Val Ala Arg Ser Asp
        115                 120                 125
Gln Val Arg Asp Val Ile Ile Ala Ala Ser Val Ala Gly Met Gly Leu
    130                 135                 140
Ala Ala Met Ser Leu Ile Gly Val Met Phe Ser Arg Asn Lys Arg Gln
145                 150                 155                 160
Lys Gln
(2) INFORMATION FOR SEQ ID NO: 4:
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 160 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear
   (vii) IMMEDIATE SOURCE:
          (A) LIBRARY: GenBank
          (B) CLONE: 1709969
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
Met Pro Ile Pro Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile Phe Arg
 1               5                  10                  15
Pro Met Tyr Ser His Trp Ala Ile Tyr Val Gly Asp Gly Tyr Val Ile
            20                  25                  30
His Leu Ala Pro Pro Ser Glu Ile Pro Gly Ala Gly Ala Ala Ser Ile
        35                  40                  45
Met Ser Ala Leu Thr Asp Lys Ala Ile Val Lys Lys Glu Leu Leu Arg
    50                  55                  60
Asp Val Ala Gly Lys Asp Lys Tyr Gln Val Asn Asn Lys His Asp Lys
65                  70                  75                  80
Glu Tyr Thr Pro Leu Pro Leu Asn Lys Ile Ile Gln Arg Ala Glu Glu
                85                  90                  95
Leu Val Gly Gln Glu Val Leu Tyr Arg Leu Thr Ser Glu Asn Cys Glu
            100                 105                 110
His Phe Val Asn Glu Leu Arg Tyr Gly Val Pro Arg Ser Asp Gln Val
        115                 120                 125
Arg Asp Thr Val Lys Val Ala Thr Val Thr Gly Val Gly Leu Ala Ala
    130                 135                 140
Leu Gly Leu Ile Gly Val Met Leu Ser Arg Asn Lys Lys Gln Lys Gln
145                 150                 155                 160
```

VERIFICATION SUMMARY
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DATE: 04/17/2002
TIME: 11:53:17

Input Set : N:\Crf3\RULE60\10020618.raw
Output Set: N:\CRF3\04172002\J020618.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1